

SEQUENCE LISTING

<110> Meyers, Rachel
Hunter, John Joseph

<120> 62112, A NOVEL HUMAN DEHYDROGENASE AND
USES THEREOF

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<151> 2000-08-31

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<212> DNA

<213> Homo sapiens

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<222> (67)...(1932)

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Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala
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cgt gcc tgc cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg 156
Arg Ala Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu
15 20 25 30

cgc acc agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc 204
Arg Thr Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly
35 40 45

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Lys Ile Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp
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Glu Leu Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe
65 70 75

act gaa gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca 348
Thr Glu Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro
80 85 90

gat gaa act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa 396
Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln
95 100 105 110

gtc cca gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca 444
Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser
115 120 125

aga cta ggg gag atc atc agc atg gat ggg tcc atc act gtg acc ctg Arg Leu Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu	492
130 135 140	
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145 150 155	
gag gag cag aaa gcc aaa tac ttg cct aaa ctg gcg tcc ggg gag cac Glu Glu Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His	588
160 165 170	
att gca gcc ttc tgc ctc acg gag cca gcc agt ggg agc gat gca gcc Ile Ala Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala	636
175 180 185 190	
tca atc cgg agc aga gcc aca cta agt gaa gac aag aag cac tac atc Ser Ile Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile	684
195 200 205	
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255 260 265 270	
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320 325 330	
agg ctc agt gaa ttt gga ttg att cag gag aaa ttt gca ctg atg gct Arg Leu Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala	1116
335 340 345 350	
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355 360 365	
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Gln Ile Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg		
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Ile Leu Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr		
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Val Met Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr		
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Gln Leu Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly		
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cgc aac cac gac cac gag gtt ctc ttg gcc aac acc ttc tgc gtg gaa		1788
Arg Asn His Asp His Glu Val Leu Leu Ala Asn Thr Phe Cys Val Glu		
560	565	570
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Ala Tyr Leu Gln Asn Leu Phe Ser Leu Ser Gln Leu Asp Lys Tyr Ala		
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590		
cca gaa aac cta gat gag cag att aag aaa gtg tcc cag cag atc ctt		1884
Pro Glu Asn Leu Asp Glu Gln Ile Lys Lys Val Ser Gln Gln Ile Leu		
595	600	605
gag aag cga gcc tat atc tgt gcc cac cct ctg gac agg aca tgc tga		1932
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610

615

620

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Asn	Glu	Ile	Asn	Gln	Phe	Leu	Gly	Pro	Val	Glu	Lys	Phe	Phe	Thr	Glu
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						100			105					110	
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Gly	Glu	Ile	Ile	Ser	Met	Asp	Gly	Ser	Ile	Thr	Val	Thr	Leu	Ala	Ala
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His	Gln	Ala	Ile	Gly	Leu	Lys	Gly	Ile	Ile	Leu	Ala	Gly	Thr	Glu	
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Gln	Lys	Ala	Lys	Tyr	Leu	Pro	Lys	Leu	Ala	Ser	Gly	Glu	His	Ile	Ala
						165			170					175	
Ala	Phe	Cys	Leu	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Asp	Ala	Ala	Ser	Ile
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Arg	Ser	Arg	Ala	Thr	Leu	Ser	Glu	Asp	Lys	His	Tyr	Ile	Leu	Asn	
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Ser Ala Asn Lys Phe Glu Glu Asn	Thr Tyr Cys Phe Gly Arg	Thr Val
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Glu Thr Leu Leu Leu Arg Phe	Gly Lys Thr Ile Met	Glu Glu Gln Leu
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Leu Gln Asn Leu Phe Ser Leu Ser	Gln Leu Asp Lys Tyr	Ala Pro Glu
580	585	590
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.
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Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
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agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc aaa atc 144
Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
   35          40          45

aag aag aaa gaa gtt ttc cca ttt cca gaa gtt agc caa gat gaa ctt 192
Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu

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50

55

60

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85 90 95	
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100 105 110	
gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca aga cta Glu Glu Tyr Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu	384
115 120 125	
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130 135 140	
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145 150 155 160	
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165 170 175	
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180 185 190	
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245 250 255	
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260 265 270	
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Gln Pro Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met Val Lys Val			
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530	535	540	

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Ala Val Leu Ser Arg	Ala Ser Arg Ser Ile	Arg Ile Gly	Leu Arg Asn	
545	550	555	560	
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His Asp His Glu Val	Leu Ala Asn Thr	Phe Cys Val Glu	Ala Tyr	
565	570	575		
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Leu Gln Asn Leu Phe	Ser Leu Ser Gln	Leu Asp Lys Tyr	Ala Pro Glu	
580	585	590		
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Asn Leu Asp Glu Gln	Ile Lys Lys Val	Ser Gln Gln	Ile Leu Glu Lys	
595	600	605		
cga gcc tat atc tgt	gcc cac cct ctg	gac agg aca tgc		1863
Arg Ala Tyr Ile Cys	Ala His Pro Leu Asp	Arg Thr Cys		
610	615	620		

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